

T0330X

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Campbell, Robert K.
Jameson, Bradford A.
Chappel, Scott C.

(ii) TITLE OF INVENTION: HYBRID PROTEINS

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BROWDY AND NEIMARK
(B) STREET: 419 Seventh Street N.W., Ste. 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 22207

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/011,936
(B) FILING DATE: 20 February 1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Browdy, Roger L.
(B) REGISTRATION NUMBER: 25,618
(C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 628-5197
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 278..1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG | 60 |
| AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTCTCAAT | 120 |
| CTCACTATCG CCATGTAAGC CCAGTATTTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA | 180 |
| GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT | 240 |
| CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC | 295 |
| Ser Arg Thr Ser Leu Leu | |
| 1 5 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CTG | GCT | TTT | GGC | CTG | CTC | TGC | CTG | CCC | TGG | CTT | CAA | GAG | GGC | AGT | GCC | 343 |
| Leu | Ala | Phe | Gly | Leu | Leu | Cys | Leu | Pro | Trp | Leu | Gln | Glu | Gly | Ser | Ala | |
| | | | 10 | | | | | 15 | | | | | 20 | | | |
| GAT | AGT | GTG | TGT | CCC | CAA | GGA | AAA | TAT | ATC | CAC | CCT | CAA | AAT | AAT | TCC | 391 |
| Asp | Ser | Val | Cys | Pro | Gln | Gly | Lys | Tyr | Ile | His | Pro | Gln | Asn | Asn | Ser | |
| | | 25 | | | | | 30 | | | | | 35 | | | | |
| ATT | TGC | TGT | ACC | AAG | TGC | CAC | AAA | GGA | ACC | TAC | TTG | TAC | AAT | GAC | TGT | 439 |
| Ile | Cys | Cys | Thr | Lys | Cys | His | Lys | Gly | Thr | Tyr | Leu | Tyr | Asn | Asp | Cys | |
| | 40 | | | | | 45 | | | | | 50 | | | | | |
| CCA | GGC | CCG | GGG | CAG | GAT | ACG | GAC | TGC | AGG | GAG | TGT | GAG | AGC | GGC | TCC | 487 |
| Pro | Gly | Pro | Gly | Gln | Asp | Thr | Asp | Cys | Arg | Glu | Cys | Glu | Ser | Gly | Ser | |
| | 55 | | | | 60 | | | | | 65 | | | | | 70 | |
| TTC | ACC | GCT | TCA | GAA | AAC | CAC | CTC | AGA | CAC | TGC | CTC | AGC | TGC | TCC | AAA | 535 |
| Phe | Thr | Ala | Ser | Glu | Asn | His | Leu | Arg | His | Cys | Leu | Ser | Cys | Ser | Lys | |
| | | | | 75 | | | | | 80 | | | | | 85 | | |
| TGC | CGA | AAG | GAA | ATG | GGT | CAG | GTG | GAG | ATC | TCT | TCT | TGC | ACA | GTG | GAC | 583 |
| Cys | Arg | Lys | Glu | Met | Gly | Gln | Val | Glu | Ile | Ser | Ser | Cys | Thr | Val | Asp | |
| | | | 90 | | | | | 95 | | | | | 100 | | | |
| CGG | GAC | ACC | GTG | TGT | GGC | TGC | AGG | AAG | AAC | CAG | TAC | CGG | CAT | TAT | TGG | 631 |
| Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | Lys | Asn | Gln | Tyr | Arg | His | Tyr | Trp | |
| | | 105 | | | | | 110 | | | | | 115 | | | | |
| AGT | GAA | AAC | CTT | TTC | CAG | TGC | TTC | AAT | TGC | AGC | CTC | TGC | CTC | AAT | GGG | 679 |
| Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | Asn | Cys | Ser | Leu | Cys | Leu | Asn | Gly | |
| | 120 | | | | | 125 | | | | | 130 | | | | | |
| ACC | GTG | CAC | CTC | TCC | TGC | CAG | GAG | AAA | CAG | AAC | ACC | GTG | TGC | ACC | TGC | 727 |
| Thr | Val | His | Leu | Ser | Cys | Gln | Glu | Lys | Gln | Asn | Thr | Val | Cys | Thr | Cys | |
| | 135 | | | | 140 | | | | | 145 | | | | | 150 | |
| CAT | GCA | GGT | TTC | TTT | CTA | AGA | GAA | AAC | GAG | TGT | GTC | TCC | TGT | GCC | GGT | 775 |
| His | Ala | Gly | Phe | Phe | Leu | Arg | Glu | Asn | Glu | Cys | Val | Ser | Cys | Ala | Gly | |
| | | | 155 | | | | | | 160 | | | | | 165 | | |
| GCT | GCC | CCA | GGT | TGC | CCA | GAA | TGC | ACG | CTA | CAG | GAA | AAC | CCA | TTC | TTC | 823 |
| Ala | Ala | Pro | Gly | Cys | Pro | Glu | Cys | Thr | Leu | Gln | Glu | Asn | Pro | Phe | Phe | |
| | | | 170 | | | | | 175 | | | | | 180 | | | |
| TCC | CAG | CCG | GGT | GCC | CCA | ATA | CTT | CAG | TGC | ATG | GGC | TGC | TGC | TTC | TCT | 871 |
| Ser | Gln | Pro | Gly | Ala | Pro | Ile | Leu | Gln | Cys | Met | Gly | Cys | Cys | Phe | Ser | |
| | | 185 | | | | | 190 | | | | | 195 | | | | |
| AGA | GCA | TAT | CCC | ACT | CCA | CTA | AGG | TCC | AAG | AAG | ACG | ATG | TTG | GTC | CAA | 919 |
| Arg | Ala | Tyr | Pro | Thr | Pro | Leu | Arg | Ser | Lys | Lys | Thr | Met | Leu | Val | Gln | |
| | 200 | | | | | 205 | | | | | 210 | | | | | |
| AAG | AAC | GTC | ACC | TCA | GAG | TCC | ACT | TGC | TGT | GTA | GCT | AAA | TCA | TAT | AAC | 967 |
| Lys | Asn | Val | Thr | Ser | Glu | Ser | Thr | Cys | Cys | Val | Ala | Lys | Ser | Tyr | Asn | |
| | 215 | | | | 220 | | | | | 225 | | | | | 230 | |
| AGG | GTC | ACA | GTC | ATG | GGG | GGT | TTC | AAA | GTG | GAG | AAC | CAC | ACG | GGG | TGC | 1015 |
| Arg | Val | Thr | Val | Met | Gly | Gly | Phe | Lys | Val | Glu | Asn | His | Thr | Gly | Cys | |
| | | | | 235 | | | | | 240 | | | | | 245 | | |
| CAC | TGC | AGT | ACT | TGT | TAT | TAT | CAC | AAA | TCT | TA | AG | | | | | 1049 |
| His | Cys | Ser | Thr | Cys | Tyr | Tyr | His | Lys | Ser | | | | | | | |
| | | | 250 | | | | | 255 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
115 120 125
Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
130 135 140
Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
145 150 155 160
Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
165 170 175
Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
180 185 190
Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
195 200 205
Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
210 215 220
Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
225 230 235 240
Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 279..1199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----------------|
| CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG | 60 |
| GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA | 120 |
| TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG | 180 |
| AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC | 240 |
| TCCGGCTCCC TCTGTTGCCC TGTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG | 293 |
| Ser Arg Thr Ser Leu | 260 |
| CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT | 341 |
| Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser | 265 270 275 |
| GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT | 389 |
| Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn | 280 285 290 |
| TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC | 437 |
| Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp | 295 300 305 |
| TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC | 485 |
| Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly | 310 315 320 325 |
| TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC | 533 |
| Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser | 330 335 340 |
| AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG | 581 |
| Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val | 345 350 355 |
| GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT | 629 |
| Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr | 360 365 370 |
| TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT | 677 |
| Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn | 375 380 385 |
| GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC | 725 |
| Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr | 390 395 400 405 |
| TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCT | 773 |
| Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala | 410 415 420 |
| GGT GCT GGT CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG | 821 |
| Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu | 425 430 435 |
| AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC | 869 |
| Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala | 440 445 450 |

| | |
|---|------|
| GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTC CCC GCC | 917 |
| Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala | |
| 455 460 465 | |
| CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC | 965 |
| Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile | |
| 470 475 480 485 | |
| CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCT | 1013 |
| Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala | |
| 490 495 500 | |
| GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC | 1061 |
| Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp | |
| 505 510 515 | |
| TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC | 1109 |
| Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Pro Arg Phe | |
| 520 525 530 | |
| CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA | 1157 |
| Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro | |
| 535 540 545 | |
| TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA TAA | 1202 |
| Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln | |
| 550 555 560 | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Thr | Ser | Leu | Leu | Leu | Ala | Phe | Gly | Leu | Leu | Cys | Leu | Pro | Trp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Gln | Glu | Gly | Ser | Ala | Asp | Ser | Val | Cys | Pro | Gln | Gly | Lys | Tyr | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Pro | Gln | Asn | Asn | Ser | Ile | Cys | Cys | Thr | Lys | Cys | His | Lys | Gly | Thr |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Tyr | Leu | Tyr | Asn | Asp | Cys | Pro | Gly | Pro | Gly | Gln | Asp | Thr | Asp | Cys | Arg |
| | 50 | | | | 55 | | | | | | 60 | | | | |
| Glu | Cys | Glu | Ser | Gly | Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu | Arg | His |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Cys | Leu | Ser | Cys | Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val | Glu | Ile |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ser | Ser | Cys | Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | Lys | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gln | Tyr | Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | Asn | Cys |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Ser | Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu | Lys | Gln |
| | | | 130 | | | | 135 | | | | | 140 | | | |

Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
 145 150 155 160
 Cys Val Ser Cys Ala Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala
 165 170 175
 Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn
 180 185 190
 Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln
 195 200 205
 Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val
 210 215 220
 Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro
 225 230 235 240
 Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg
 245 250 255
 Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys
 260 265 270
 Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro
 275 280 285
 Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
 290 295 300
 Leu Pro Gln
 305

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 278..1132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| TCGAGATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG | 60 |
| AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCTT CAGGTTTGGG GCTTTTGAAT | 120 |
| GTGAGTATGG CCATGTAAGC CCAGTATTTG CCCAATCTCA GAAAGCTCCT GGTCCCTGGA | 180 |
| GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA CACTCCTGGC CTCTTGCTCT | 240 |
| GCGGCTCCGT GTGTTGCCCT GTGGTTTCTC CCCACGC TCC CGG ACG TCC CTG CTC | 295 |
| Ser Arg Thr Ser Leu Leu | 310 |
| CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC | 343 |
| Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala | |
| 315 320 325 | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|------------|-------------------|------|
| GAT Asp 330 | AGT Ser | GTG Val | TGT Cys | CCC Pro | CAA Gln 335 | GGA Gly | AAA Lys | TAT Tyr | ATC Ile | CAC His 340 | CCT Pro | CAA Gln | AAT Asn | AAT Asn | TCG Ser 345 | 391 |
| ATT Ile | TGC Cys | TGT Cys | ACC Thr | AAG Lys 350 | TGC Cys | CAC His | AAA Lys | GGA Gly | ACC Thr | TAC Tyr | TTG Leu | TAC Tyr | AAT Asn | GAC Asp | TGT Cys 360 | 439 |
| CCA Pro | GGC Gly | CCG Pro | GGG Gly 365 | CAG Gln | GAT Asp | ACC Thr | GAC Asp | TGC Cys 370 | AGG Arg | GAG Glu | TGT Cys | GAG Glu | AGC Ser | GGC Gly | TCC Ser | 487 |
| TTC Phe | ACC Thr | GCT Ala 380 | TCA Ser | GAA Glu | AAC Asn | CAC His | CTC Leu 385 | AGA Arg | CAC His | TGC Cys | CTC Leu | AGC Ser | TGC Cys | TCC Ser | AAA Lys | 535 |
| TGC Cys | CGA Arg 395 | AAG Lys | GAA Glu | ATG Met | GGT Gly | CAG Gln 400 | GTG Val | GAG Glu | ATC Ile | TCT Ser | TCT Ser | TGC Cys | ACA Thr | GTG Val | GAC Asp | 583 |
| CGG Arg 410 | GAC Asp | ACC Thr | GTG Val | TGT Cys | GGC Gly 415 | TGC Cys | AGG Arg | AAG Lys | AAC Asn | CAG Gln 420 | TAC Tyr | CGG Arg | CAT His | TAT Tyr | TGG Trp 425 | 631 |
| AGT Ser | GAA Glu | AAC Asn | CTT Leu | TTC Phe 430 | CAG Gln | TGC Cys | TTC Phe | AAT Asn | TGC Cys 435 | ACC Thr | CTC Leu | TGC Cys | CTC Leu | AAT Asn | GGG Gly 440 | 679 |
| ACC Thr | GTG Val | CAC His | CTC Leu | TCC Ser 445 | TGT Cys | CAG Gln | GAG Glu | AAA Lys | CAG Gln | AAC Asn | ACC Thr | GTC Val | TGC Cys | ACC Thr | TGC Cys | 727 |
| CAT His | GCA Ala 460 | GGT Gly | TTC Phe | TTT Phe | CTA Leu | AGA Arg | GAA Glu 465 | AAC Asn | GAG Glu | TGT Cys | GTC Val | TCC Ser | TGT Cys | AGT Ser | AAC Asn | 775 |
| TGT Cys | AAG Lys 475 | AAA Lys | AGC Ser | CTG Leu | GAG Glu | TGC Cys | ACG Thr | AAG Lys | TTG Leu | TCC Ser | CTA Leu | CCC Pro | CAG Gln | ATT Ile | GAG Glu | 823 |
| AAT Asn 490 | GTT Val | AAG Lys | GGC Gly | ACT Thr | GAG Glu 495 | GAC Asp | TCA Ser | GGC Gly | ACC Thr | ACA Thr 500 | GCC Ala | GGT Gly | GCT Ala | GCC Ala | CCA Pro 505 | 871 |
| GGT Gly | TGC Cys | CCA Pro | GAA Glu | TGC Cys 510 | ACG Thr | CTA Leu | CAG Gln | GAA Glu | AAC Asn 515 | CCA Pro | TTC Phe | TTC Phe | TCC Ser | CAG Gln | CCG Pro 520 | 919 |
| GGT Gly | GCC Ala | CCA Pro | ATA Ile 525 | CTT Leu | CAG Gln | TGC Cys | ATG Met | GGC Gly 530 | TGC Cys | TGC Cys | TTC Phe | TCT Ser | AGA Arg 535 | GCA Ala | TAT Tyr | 967 |
| CCC Pro | ACT Thr | CCA Pro | CTA Leu | AGG Arg | TCC Ser | AAG Lys | AAG Lys | ACG Thr | ATG Met | TTG Leu | GTC Val | CAA Gln 550 | AAG Lys | AAC Asn | GTC Val | 1015 |
| ACC Thr 555 | TCA Ser | GAG Glu | TCC Ser | ACT Thr | TGC Cys | TGT Cys | GTA Val | GCT Ala | AAA Lys | TCA Ser | TAT Tyr | AAC Asn | AGG Arg | GTC Val | ACA Thr | 1063 |
| GTA Val 570 | ATG Met | GGG Gly | GGT Gly | TTC Phe | AAA Lys 575 | GTG Val | GAG Glu | AAC Asn | CAC His | ACG Thr 580 | GCG Ala | TGC Cys | CAC His | TGC Cys | AGT Ser 585 | 1111 |
| ACT Thr | TGT Cys | TAT Tyr | TAT Tyr | CAC His 590 | AAA Lys | TCT Ser | TAAGGATCCC TCGAG | | | | | | | | | 1147 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
115 120 125
Thr Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
130 135 140
Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
145 150 155 160
Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu
165 170 175
Ser Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
180 185 190
Thr Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn
195 200 205
Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys
210 215 220
Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met
225 230 235 240
Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys
245 250 255
Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His
260 265 270
Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
275 280 285

[illegible]

(A) LENGTH: 1301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 279..1287

| | | | | | | | |
|---|------------|-------------|------------|---------------------|-------------|--|-----|
| CTCGAGATGG | CTACAGGTAA | GCGCCCCCTAA | AATCCCTTTG | GGCACAAATGT | GTCCTGAGGG | | 60 |
| GAGAGGCAGC | GACCTGTAGA | TGGGACGGGG | GCACTAACCC | TCAGGTTTGG | GGCTTCTGAA | | 120 |
| TGTGAGTATC | GCCATGTAAG | CCCAGTATTT | GGCCAATGTC | AGAAAGCTCC | TGGTCCCCTGG | | 180 |
| AGGGATGGAG | AGAGAAAAAC | AAACACCTCC | TGGAGCAGGG | AGAGTGCTGC | CCTCTTGCTC | | 240 |
| TCCGGCTCCC | TCTGTTGCCC | TCTGGTTTCT | CCCCAGGC | TCC CGG ACG TCC CTG | | | 293 |
| | | | | Ser Arg Thr Ser Leu | | | 290 |
| CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT | | | | | | | 341 |
| Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser | | | | | | | |
| | | | | 295 | | | 300 |
| GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT | | | | | | | 389 |
| Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn | | | | | | | |
| | | | | 310 | | | 315 |
| TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC | | | | | | | 437 |
| Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp | | | | | | | |
| | | | | | | | 325 |
| TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC | | | | | | | 485 |
| Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly | | | | | | | |
| | | | | | | | 340 |
| TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC | | | | | | | 533 |
| Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser | | | | | | | |
| | | | | | | | 355 |
| AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG | | | | | | | 581 |
| Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val | | | | | | | |
| | | | | | | | 375 |
| GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT | | | | | | | 629 |
| Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr | | | | | | | |
| | | | | | | | 390 |
| TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT | | | | | | | 677 |
| Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn | | | | | | | |
| | | | | | | | 405 |
| GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC | | | | | | | 725 |
| Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr | | | | | | | |
| | | | | | | | 420 |
| TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT | | | | | | | 773 |
| Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser | | | | | | | |
| | | | | | | | 435 |

| | |
|---|------|
| AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT | 821 |
| Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile | |
| 455 460 465 | |
| GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GCT GGT GCT GGT | 869 |
| Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Ala Gly Ala Gly | |
| 470 475 480 | |
| CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG AAG GAG GGC | 917 |
| Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu Lys Glu Gly | |
| 485 490 495 | |
| TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC GGC TAC TGC | 965 |
| Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys | |
| 500 505 510 | |
| CCC ACC ATG ACC CGC GTG CTG CAG GGC GTC CTG CCG GCC CTG CCT CAG | 1013 |
| Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln | |
| 515 520 525 530 | |
| GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC CGG CTC CCT | 1061 |
| Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro | |
| 535 540 545 | |
| GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC GTG GCT CTC | 1109 |
| Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu | |
| 550 555 560 | |
| AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC TGC GGG GGT | 1157 |
| Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly | |
| 565 570 575 | |
| CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC CAG GAC TCC | 1205 |
| Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser | |
| 580 585 590 | |
| TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA TCC CGA CTC | 1253 |
| Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu | |
| 595 600 605 610 | |
| CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA T AAGGATCCCT CGAG | 1301 |
| Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln | |
| 615 620 | |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| |
|---|
| Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp |
| 1 5 10 15 |
| Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile |
| 20 25 30 |
| His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr |
| 35 40 45 |
| Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg |
| 50 55 60 |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Cys | Glu | Ser | Gly | Ser | Phe | Thr | Ala | Ser | Glu | Asn | His | Leu | Arg | His | 65 | 70 | 75 | 80 |
| Cys | Leu | Ser | Cys | Ser | Lys | Cys | Arg | Lys | Glu | Met | Gly | Gln | Val | Glu | Ile | 85 | 90 | 95 | |
| Ser | Ser | Cys | Thr | Val | Asp | Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | Lys | Asn | 100 | 105 | 110 | |
| Gln | Tyr | Arg | His | Tyr | Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | Asn | Cys | 115 | 120 | 125 | |
| Ser | Leu | Cys | Leu | Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu | Lys | Gln | 130 | 135 | 140 | |
| Asn | Thr | Val | Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu | Asn | Glu | 145 | 150 | 155 | 160 |
| Cys | Val | Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr | Lys | Leu | 165 | 170 | 175 | |
| Cys | Leu | Pro | Gln | Ile | Glu | Asn | Val | Lys | Gly | Thr | Glu | Asp | Ser | Gly | Thr | 180 | 185 | 190 | |
| Thr | Ala | Gly | Ala | Gly | Pro | Arg | Cys | Arg | Pro | Ile | Asn | Ala | Thr | Leu | Ala | 195 | 200 | 205 | |
| Val | Glu | Lys | Glu | Gly | Cys | Pro | Val | Cys | Ile | Thr | Val | Asn | Thr | Thr | Ile | 210 | 215 | 220 | |
| Cys | Ala | Gly | Tyr | Cys | Pro | Thr | Met | Thr | Arg | Val | Leu | Gln | Gly | Val | Leu | 225 | 230 | 235 | 240 |
| Pro | Ala | Leu | Pro | Gln | Val | Val | Cys | Asn | Tyr | Arg | Asp | Val | Arg | Phe | Glu | 245 | 250 | 255 | |
| Ser | Ile | Arg | Leu | Pro | Gly | Cys | Pro | Arg | Gly | Val | Asn | Pro | Val | Val | Ser | 260 | 265 | 270 | |
| Tyr | Ala | Val | Ala | Leu | Ser | Cys | Gln | Cys | Ala | Leu | Cys | Arg | Arg | Ser | Thr | 275 | 280 | 285 | |
| Thr | Asp | Cys | Gly | Gly | Pro | Lys | Asp | His | Pro | Leu | Thr | Cys | Asp | Asp | Pro | 290 | 295 | 300 | |
| Arg | Phe | Gln | Asp | Ser | Ser | Ser | Ser | Lys | Ala | Pro | Pro | Pro | Ser | Leu | Pro | 305 | 310 | 315 | 320 |
| Ser | Pro | Ser | Arg | Leu | Pro | Gly | Pro | Ser | Asp | Thr | Pro | Ile | Leu | Pro | Gln | 325 | 330 | 335 | |

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Gly Ala Ala Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Gly Ala Gly
1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTCTCGAG ATGGCTACAG GTAAGCGCCC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACCTGGGGCA GCACCGGCAC AGGAGACACA CTCGTTTTC

39

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGCCGGTG CTGCCCCAGG TTGCCAGAA TGCACGCTAC AG

42

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTGGATCC TTAAGATTTG TGATAATAAC AAGTAC 36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTGGACCA GCACCAGCAC AGGAGACACA CTCGTTTTTC 39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTGCTGGTG CTGGTCCACG GTGCCGCCCC ATCAAT 36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTTGGATCC TTATTGTGGG AGGATCGGGG TG 32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTTAGATCT CTTCTGAC AGTGGAC 27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGTGCCT GAGTCCTCAG T

21

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTGAGGACT CAGGCACCAC AGCCGGTGCT GCCCCAGGTT G

41

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTCTAGA GAAGCAGCAG CAGCCCATG

29

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTCACAG CCAGGGTGGC ATTGATGGGG CGGCACCGTG GACCAGCACC AGCTGTGGTG

60

CCTGAGTCCT CAGTG

75